Table S3. Parameters for parsimony score used in `kwarg` to reconstruct ancestral recombination graphs

Runtime per ARG	Configuration complexity	Parsimony score = $r^b + \max(am^c/maxam, seq^d/maxseq)$ + the following:
< 2 hrs	$maxlen^a > 100$	$2 \times hk^e$
	$50 < maxlen \leq 100$	$1.5 \times \max(eagl(7)^f, hb(2, 50, 6)^g)$
	$maxlen \leq 50, maxam \geq 100$	$1.25 \times \max(eagl(10), hb(2, -1, -1))$
	$maxlen \leq 50, maxam < 100$	$rmin^h$
> 2 hrs	$maxlen > 100$	$2 \times hk$
	$50 < maxlen \leq 100$	$1.5 \times \max(eagl(5), hb(2, 50, 6))$
	$maxlen \leq 50, maxam \geq 25$	$1.25 \times \max(eagl(7), hb(2, 50, 10))$
	$maxlen \leq 50, maxam < 25$	$rmin$

Shown are parameter choices used in the parsimony score at differing stages of genealogical inference by `kwarg`. At a given stage in the calculation, the set of recombination, mutation, and coalescence events inferred by previous steps determines a set of remaining sequences referred to as the *configuration*. Each row in the table represents parameter values used to calculate the parsimony score when evaluating move choices for the *next* step, at the indicated configuration complexity.

[a] The maximum number of segregating sites remaining after any proposed move.
[b] The number of recombination events in the proposed event (zero or one).
[c] The resulting length of ancestral material after the proposed step ($maxam$ is the maximum across all proposed moves).
[d] The number of sequences remaining after the proposed step ($maxseq$ is the maximum across all proposed moves).
[e] The Hudson-Kaplan lower bound on the remaining data after the proposed step.
[f] A composite lower bound combining the exact minimum across disjoint intervals.
[g] The haplotype lower bound.
[h] The exact minimum number of recombination events remaining.
Parameters for these bounds are described in Lyngsø *et al.* (2005).